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Timestamp: [year=2010; month=8; day=30; hr=10; min=48; sec=25; ms=714;]

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Application No: 10591787 Version No: 4.0

Input Set:

Output Set:

Started: 2010-08-23 17:48:50.682
Finished: 2010-08-23 17:49:02.939
Elapsed: 0 hr(s) 0 min(s) 12 sec(s) 257 ms
Total Warnings: 5
Total Errors: 0
No. of SeqIDs Defined: 91
Actual SeqID Count: 91

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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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SEQUENCE LISTING

<110> Nagaike, Kazuhiro
Mori, Yasuko
Gomi, Yasuyuki
Takahashi, Michiaki
Kouichi, Yamanishi

<120> Recombinant varicella-zoster virus

<130> 59150-8037

<140> 10591787

<141> 2010-08-23

<150> PCT/JP2005/003652

<151> 2005-03-05

<150> JP 2004-063277

<151> 2004-03-05

<160> 91

<170> PatentIn version 3.2

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<220>
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<223> The 'Xaa' at location 1275 stands for Ser, or Leu.

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acacgtttta agtactgttg gaactccctc accaaccgca aycgcaatcc tttgaaggct 180

gcgagagcgt ttggaaaact cgggtacgtc taaattcacc ccagygcg atg gat acg 237
Met Asp Thr
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ccg ccg atg cag cgc tct aca ccc caa cgc gcg ggg tcg cct gat act 285
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Leu Glu Leu Met Asp Leu Leu Asp Ala Ala Ala Ala Ala Glu His	
20 25 30 35	
agg gcc cgg gtg gtc acc tcg agt cag cct gac gat cta cta ttt gga	381
Arg Ala Arg Val Val Thr Ser Ser Gln Pro Asp Asp Leu Leu Phe Gly	
40 45 50	
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Glu Asn Gly Val Met Val Gly Arg Glu His Glu Ile Val Ser Ile Pro	
55 60 65	
tcc gta tcg gga ctt caa cca gaa ccc aga acg gaa gat gtt ggc gaa	477
Ser Val Ser Gly Leu Gln Pro Glu Pro Arg Thr Glu Asp Val Gly Glu	
70 75 80	
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Glu Leu Thr Gln Asp Asp Tyr Val Cys Glu Asp Gly Gln Asp Leu Xaa	
85 90 95	
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Gly Ser Pro Val Ile Pro Leu Ala Glu Val Phe His Thr Arg Phe Ser	
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Glu Ala Gly Ala Arg Glu Pro Thr Gly Ala Asp Arg Ser Leu Glu Thr	
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Val Ser Leu Gly Thr Lys Leu Ala Arg Ser Pro Lys Pro Pro Met Asn	
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Asp Gly Glu Thr Gly Arg Gly Thr Thr Pro Pro Phe Pro Gln Ala Phe	
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Val Leu Ser Asp Ser Val Pro Ala Lys Gly Ala Lys Ala Asp Leu Pro	
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Phe Glu Thr Asp Asp Thr Arg Pro Arg Lys His Asp Ala Arg Gly Ile	
295 300 305	
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Thr Pro Arg Val Pro Gly Arg Ser Ser Gly Gly Lys Pro Arg Ala Phe	
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Leu Ala Leu Pro Gly Arg Ser His Ala Pro Asp Pro Ile Glu Asp Asp	
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Ser Pro Val Glu Lys Lys Pro Lys Ser Arg Glu Phe Val Ser Ser Ser	
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Ser Ser Ser Ser Ser Trp Gly Ser Ser Ser Glu Asp Glu Asp Asp Glu	
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Pro Arg Arg Val Ser Val Gly Ser Glu Thr Thr Gly Ser Arg Ser Gly	
375 380 385	
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Arg Glu His Ala Pro Ser Pro Ser Asn Ser Asp Asp Ser Asp Ser Asn	
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Pro Gly Arg Gln Arg Gln Lys Ser Phe Ser Leu Pro Arg Ser Arg Thr	
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455 460 465	
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Pro Trp Pro Gly Ser Ala Pro Leu Pro Ser Asn Arg Val Arg Phe Gly	
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485 490 495	
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Ala Ala Arg Ala Arg Tyr Glu Ala Ser Thr Glu Pro Xaa Pro Leu Tyr	
500 505 510 515	
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Val Pro Glu Leu Gly Asp Pro Ala Arg Gln Tyr Arg Ala Leu Ile Asn	
520 525 530	
ctg atc tac tgt cca gac aga gac cct ata gca tgg ctc cag aac ccc	1869
Leu Ile Tyr Cys Pro Asp Arg Asp Pro Ile Ala Trp Leu Gln Asn Pro	
535 540 545	
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Lys Leu Thr Gly Val Asn Ser Ala Leu Asn Gln Phe Tyr Gln Lys Leu	
550 555 560	
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Leu Pro Pro Gly Arg Ala Gly Thr Ala Val Thr Gly Ser Val Ala Ser	
565 570 575	
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Ala Leu Pro His Ala Ala Ala Ala Val Ala Met Ser Arg Arg Tyr Asp	
600 605 610	
cgg gcc caa aaa cac ttt atc cta cag agt ctc cgc aga gcc ttt gcc	2109
Arg Ala Gln Lys His Phe Ile Leu Gln Ser Leu Arg Arg Ala Phe Ala	
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Ser Arg Gly His Pro Ser Pro Thr Thr Pro Ala Thr Gln Thr Pro Asp	
645 650 655	
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Pro Gln Pro Ser Ala Ala Ala Arg Ser Leu Ser Val Cys Pro Pro Asp	
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Asp Arg Leu Arg Thr Pro Arg Lys Arg Lys Ser Gln Pro Val Glu Ser	
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Pro Val Thr Ile Thr Ser Gly Pro Val Val Asp Pro Pro Ala Val Ile			
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Thr Met Pro Leu Asp Gly Pro Ala Pro Asn Gly Gly Phe Arg Arg Ile			
740	745	750	755
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Pro Arg Gly Ala Leu His Thr Pro Val Pro Ser Asp Gln Ala Arg Lys			
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Ala Tyr Cys Thr Pro Glu Thr Ile Ala Arg Leu Val Asp Asp Pro Leu			
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Phe Pro Thr Ala Trp Arg Pro Ala Leu Ser Phe Asp Pro Gly Ala Leu			
790	795	800	
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Ala Glu Ile Ala Ala Arg Arg Pro Gly Gly Gly Asp Arg Arg Phe Gly			
805	810	815	
cca ccc agc gga gtg gag gcg ctg cga cgg agg tgc gcc tgg atg cgg			2733
Pro Pro Ser Gly Val Glu Ala Leu Arg Arg Arg Cys Ala Trp Met Arg			
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Gln Ile Pro Asp Pro Glu Asp Val Arg Leu Leu Ile Ile Tyr Asp Pro			
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Leu Pro Gly Glu Asp Ile Asn Gly Pro Leu Glu Ser Thr Leu Ala Thr			
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Asp Pro Gly Pro Ser Trp Ser Pro Ser Arg Gly Gly Leu Ser Val Val			
870	875	880	
ctg gca gcc ctg agt aac cgg ttg tgc ctg ccg agc act cat gcc tgg			2925
Leu Ala Ala Leu Ser Asn Arg Leu Cys Leu Pro Ser Thr His Ala Trp			
885	890	895	
gcc ggg aac tgg acc ggc ccg ccg gac gtg tcc gct ttg aac gcc cgg			2973
Ala Gly Asn Trp Thr Gly Pro Pro Asp Val Ser Ala Leu Asn Ala Arg			
900	905	910	915
ggc gtt tta tta ctg tcg acc cga gac ctg gcc ttt gcc ggg gcc gtc			3021
Gly Val Leu Leu Leu Ser Thr Arg Asp Leu Ala Phe Ala Gly Ala Val			
920	925	930	

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Leu Asp Ala Val Ala Leu Glu Arg Trp Pro Gly Asp Gly Pro Ala Leu	
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Ser Gln Tyr His Val Tyr Val Arg Ala Pro Ala Arg Pro Asp Ala Gln	
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Ser	Ala	Asp	Glu	Ala	Arg	Asn	Ala	Leu	Pro	Pro	Ile	Pro	Arg	Val	
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